157 Long-term impact of fungi on pediatric cystic fibrosis lung disease

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Background and Objectives: Fungi, particularly *Aspergillus* and *Candida* species, are increasingly found in cystic fibrosis (CF) airway fluids. However, their association with other CF pathogens, medications and lung function, especially in CF children, remains elusive. We analyzed the relationship of fungal colonization to microbiological and clinical parameters of pediatric CF patients.
Methods and Results: Fungal colonization and long-term clinical parameters like BMI and lung function were retrospectively studied in over 500 CF patients. Colonization was defined based on Chotirmall et al. (Chest 2010). *Candida albicans* (CA) was the most prevalent fungus detected in CF airway fluids, followed by *C.* non-*albicans* > *Aspergillus fumigatus* (AF) > *A.* non-*fumigatus* species. We found an association between fungal colonization and (among other parameters) bacterial co-colonization, lung function, BMI and antibiotic therapy.
Conclusion: This study suggests that colonization with CA or AF is affected by bacterial co-colonization and may modulate the disease severity already in pediatric CF patients.

158 Prevalence of *Pneumocystis jirovecii* in a cross section of patients attending a large UK adult cystic fibrosis centre

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Objectives: *Pneumocystis jirovecii* is an atypical fungus that causes pneumonia in immunocompromised patients. Its role in patients with CF is unclear. Its reported prevalence in CF ranges from 1–22% but has never been determined in UK centres. Here we present preliminary cross sectional data from an ongoing study at a single UK adult CF centre serving over 400 patients, in order to establish potential risk and protective factors for infection.
Methods: Sputum samples were obtained from randomly selected CF patients and sent for routine microbiology and *Pneumocystis* PCR assay. Symptom scores, spirometry and inflammatory markers were measured and prophylactic and recent antibiotic therapy data recorded.
Results: To date, 36 patients have been recruited. The mean age was 29.9±10.6 years, mean % predicted FEV1 52.1±17.0%. Chronic infecting organisms included *P. aeruginosa* (64% of patients), *S. aureus* (44%), *B. cepacia* complex (17%), *Ralstonia* spp. (6%) and *M. abscessus* (6%). Prophylactic azithromycin was taken by 28 (78%) of patients, 9 patients 25%) had received co-trimoxazole in the previous 3 months. Only 3 patients (8%) were neither on prophylactic azithromycin nor received co-trimoxazole in the past 3 months. 1 subject had a weakly positive PCR, 2 subjects' samples were inhibitory for PCR and the remaining 33 subjects had negative PCR results.
Conclusion: Current patient numbers are small but preliminary results suggest that *Pneumocystis jirovecii* is not an important infecting pathogen in our cohort of patients. This may be due to frequent use co-trimoxaxole for pulmonary exacerbations and high prevalence of prophylactic azithromycin at our centre compared to published studies.

159 Genotyping of *Achromobacter xylosoxidans* in a cystic fibrosis (CF) centre

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Background: *A. xylosoxidans* is increasingly isolated from CF sputa. Few data on A. xylosoxidans genotype comparison between CF patients exist.
Methods: We isolated and genotyped a total of 46 *A. xylosoxidans* isolates, cultured from the sputum of 12 CF patients at the Ghent University Hospital, over a time span of one year. Genotyping was carried out by means of McRAPD and a total of 13 different genotypes were established.
Results: Eight patients harboured isolates of only one genotype, 3 patients harboured 2 genotypes, and one patient harboured 3 genotypes. Two clusters were demonstrated, cluster 1 with four patients and cluster 2 with two patients. The one patient with 3 genotypes, harboured one isolate with a unique genotype, two isolates belonging to cluster 1 and four isolates belonging to cluster 2. Overall, five out of 12 patients shared identical *A. xylosoxidans* isolates.
Conclusion: Nearly half of our patients shared a *A. xylosoxidans* genotype with one or more other patients. These results indicate possible interpatient transmission or acquisition from a common (environmental?) source.

160 Molecular profiling demonstrates clustering of *Mycobacterium abscessus* isolates in CF patients from a single centre

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Objectives: The *Mycobacterium abscessus* complex is an emerging group of pathogens in CF, which may cause cross infection. Here we present results from molecular profiling of *M. abscessus* complex isolates from patients attending a single UK adult CF centre.
Methods: Isolates were from 12 patients who yielded 1 or more positive sputum cultures for *M. abscessus* complex between January 2010 and August 2013. Isolates were identified to subspecies level using *hsp65-rpoB* concatenated sequence cluster analysis. Variable Number Tandem Repeat (VNTR) analysis was used to compare these isolates and determine whether 2 or more patients were infected with the same strain.
Results: 11 isolates were identified as *M. abscessus* subsp. *abscessus*. VNTR analysis demonstrated 2 clusters of 6 and 2 patients carrying the same strains of *M. abscessus* subsp. *abscessus*, both of which have also been isolated from CF patients from other UK hospitals. Isolates from the remaining 3 patients were unique. 1 additional isolate was identified as *M. abscessus* subsp. *bolletii*. No clear epidemiological connection between patients within each cluster at our centre has been identified to date.
Conclusion: These results provide further evidence that some strains of *M. abscessus* complex may be isolated from multiple CF patients. However, there were no clear epidemiological connections between patients within clusters at our centre. The same strains have been isolated from patients at different UK CF centres. Further studies are required to determine the mode of acquisition of infection with these strains, and whether there is a common environmental source of infection or cross infection between patients.